

FIG. 1A

1 AAGCTTTCTTGGCCCCCTAACAGCAACCACATTATACTCTTACTGGCTATTCTTGGCCTT 60
61 CAATACCCAGCCCAGGGGACCCCTCTTCCAGGGAGCCCCGCTTGTA CTCTGAGATGTCA 120
121 TGTCTTCTTGCAGAGCTCTTCCTCACGGCATCGGGACGGCGGTTACCCCTTTTGCCTCT 180
181 CCGGATAAACTGTAAGCTACTTGAGAGCAGAGAACATCCATTGTTCGCTGTGGCATCCGT 240
241 GGTACCTAGCACGGCATCTGACATATTATCAGATCTTCCACAAAGGCCAGTTTACGGTTG 300
301 AATGCCCCGTTGAATTCAAGCTCCCAGTGGGAGAGCGAGGAAGTAATAAAGCCGGTGATAA 360
361 ATGCCGCCGTGGAGACACCAGCGGGCTGCCGTGAGACTAATGGAGAGGACAGTAACGTTA 420
421 TCTCTAATGCGAGGGTGGTTATAGAGTACATTTTCATAACACCTTTAAAGCTCTTTCACAC 480
481 GCATTATCCAATTTGATCCTCATAAAAGCCTGGAGATGTGTATATTGTGGTGGATGGAGG 540
541 GGGAGTCTTTAGCAGTTATGGGATATGCCTGAAGTCGTGCAGCTAGTAAATGGCTGGATT 600
601 CAAACCAGACCTCAAAGCCTGCCTGTTTGCTCATGCCCCCTGCCCCGACTGCCCACTCT 660
661 GTGGCCACAGCACAACTCACCGTCGCTTTCTTGATCCGTTTTCTTGATCCGGCTGTGCT 720
721 CTCCCCAAGGAATGCTTTTCATTAACATATGTCTAGGTAATGAATTATCTTGACTCTGAG 780
781 GAGGCCATAGCACATGCCGTAACGCGACAGCTCCTTTGATCTGCATCTGAGGCTGTGGCT 840
841 GGTAACGGGCGTGGGGAGGGGCGTTGCTGAGACCCCAGGGACACGCCATGTGTGGTTC 900
901 CCTCTGTTTCCAGGCCCCAGAAGCACATCCCGGAAAGGAAAATGCGCTGTGGACCCCTGT 960
M R C G P L C
961 GCCGATTCTGTGGCTTTGGCCTATCTGTCTACGTTGAAGCCGTGCCCATCTGGAGAG 1020
R F L L A L A Y L S Y V E A V P I W R V
1021 TCCAGGATGACACCAAAACCCTCATCAAGACGATTGTCACCAGGATCAGTGACATTTTAC 1080
Q D D T K T L I K T I V T R I S D I S H
1081 ACATGGTAGGGAAGGCCTGGGAGACAAGGTGGAACCTGTGGCCAGCCCSGGGGGAGGAGG 1140
M
1141 GGTACCGGACCTCAGAGGTTGGCGGAGGTGGGAAGGGTCGGCGGTGGCCTTGACGCCTCC 1200
1201 CCCACCCCCCCCAACCAGCTGCCTTTGCTCCTCCGCTTCCCTCACCGCACCCCCCACGT 1260
1261 CCTTATCCTCCTTCTTCCCAGACTGGAATCCTGATGCCCAGGACTAGAGGAAGCCCTAAA 1320
1321 GGTCTGTGTGCCTTTGCCAGGTGCGCAGACCCCCCAGCATCATCCCTCTGGCCTCCAT 1380
1381 CACGTCTCCGGAATGTTCTAATCTGTAGGAATCTTCTCTGGTGACAGCTGAACTCTGACC 1440
1441 CTGCGGACGCCCCCTTACTGCTAGTCCTGCCCATTGAGCCTTTTTTCTATACAACCCTCT 1500
1501 ACATGTTTGCAAACCTTCTCTCAATGTCCCCAGGGTGTTTTCTCTGGGGTCCGCAGGCCGA 1560
1561 GACCTTCAGCCTCTTCTCAGCTGAGGTCCGTCTTTAGAATTCAGAAGACGAGGTGTGACT 1620
1621 CCTCACCTGCTGTTCCCTCTCTGTAAATCTCAAGCACGTTAAGTCCCTCCGTGTCTGA 1680
1681 AACCTTAGTTTCCCTCATCCAGATAATGGGACTGTTACTGGGAAGATGTTACCGGAATCC 1740
1741 AGGGTCTTGCTCATGGAGCTCAAGAATGAACTTGCGAACGCACAGGGAGCCGAGCAAG 1800

09932888 082001

FIG. 1B

1801	CAGAAGTCTTTATTACAGGAAGGCAGACAGCTCCCAGCACAGACACGGGGAGGGGAAGAGT	1860
1861	CCCCCGCCCATTGTTCTACGGAGGTTTTTATCACTTAAAGACGGGAGTACCAATGTGGG	1920
1921	GTCCAGATATCCGTTCTTCTTCCCATTGCCAGTTTACCTATATGGCGCCTTGTCAGGA	1980
1981	GGGACTCTGTAGAGTTAGGGGTGCTCCGTAAGTTTTATGGTGCGTCTGCTCTTCTCTGCC	2040
2041	CTAGACTTAGAGTCGCCACTCTTTCCATTCTTCTGCTCACAGTCAAATGCATAGGTCAGG	2100
2101	GGTTAATTCCACCTTCACAGAAATCAAATGTCCTTTCAATAGTTAATCTTCCAATAAGC	2160
2161	AAGGCCTGCTTGTCTTGATTAGTTTTTACAAATCTTAAACCATGGCCATTAATCAGGGAA	2220
2221	GAGATCGAAGCCCATGTTCCACACTAAGTGCCTGAATTATTAGTCTGCCTCAGGACTAT	2280
2281	CTTAATAGTCTTCGCAAGGTTGTTTTGAGATTAAATTAGATAGGAGTTCCTGTGAGGCG	2340
2341	CGACGGAAACAGATCCGACTCAGAACCATGAGACAGGTCGATCCCTGGCTTTGTCAAGT	2400
2401	GGTTAGGATCTGGTGCTGCTGTGAGCTGTGGTGTAGGTCGCAGAGGTGGCTCGGATCCCG	2460
2461	CGTTGCTGTGGCTGTGGTGTAGGCCGGTGACAGAGCTCCGATTAGACCCCTAGCCTGGG	2520
2521	AACCTCCATGTGCCGCGGGTACCGCTAAAAAAGACAAAAAGATGGAAAAAAGGTTA	2580
2581	CATTAGATAAAGCAAGTGACTCCTCCACCACCACACATATCCCTGCAGAACCAGGACAGA	2640
2641	GCATGCCTTCTTGAAAAGTTTTCGGTTGTGGCTTTGATAGCACCCAGCCTTAAAGCCAG	2700
2701	CTTTTCAATCTGCCCAGAGCAGTCTGGAGACTTCCGCATCTCCTGGCCACTCTGAGTTTC	2760
2761	TAACAGTGGCCTTGCGGAGCCTGGGAGCAGTCCGGTGGCCAGAAGCAGGGACAGCTGAGA	2820
2821	ACCAGATAGAGTCTTGGCACCTTCAAGAGAAAAACCCTAAGTCTCCTTCTTCAGCCATGC	2880
2881	AACAGCTGCGCATGACAGATCCAGCGTGTCCCAGCCTGTGTGGTGCAGGGAGTGAYGCTG	2940
2941	CGNNYAGGGYGYGGGGAGCTGAGGAGCGAGGCGGGGCATCGNGGGGCTGCAGCCTCCAT	3000
3001	CCCTAAGTGGGGAGACTTCATGAAGAGCCTGACCAGNAGGGAGGGGCATGTGTGGAGGAC	3060
3061	CTCAGGGCCTGGGGAAGGCTAGACCCAACTATGTGAGAAACAGACAGTCGTGGCTGGTTC	3120
3121	TACAGAAGAGGCATCTGGAGGCCATTGGAATGCCCAAAGCTGTCTGGGTGAGGCAGGGCT	3180
3181	TGCTAGGCAGAAGACAGAAGGCCGTGAGACCAGCTTGGAGGCTTGGCAGCCACGCCAGCC	3240
3241	CAAGGAGTTCGGGCCTAGATAGGATTGTGTGGAAGGGGAAGAGGCAGCCGAGGTGGGGG	3300
3301	GTGGGGGTGGACCCGTCTCCACGCCTGCAGGAAGGCCAGGGGCTGCAGAGCCAACATCTC	3360
3361	TCTCGCTGAGCGTCTCGCTCTCCCCCTTCTCCTGCACAGCAGTCTGTCTCCTCCAAACAG	3420
	Q S V S S K Q	
3421	AGGGTCACCGGTTTGGACTTCATCCCTGGGCTCCATCCTGTCTGAGTTTGTCCAAGATG	3480
	R V T G L D F I P G L H P V L S L S K M	
3481	GACCAGACCCTGGCGATCTACCAACAGATCCTCACCAGTCTGCCTTCCAGAAATGTGATC	3540
	D Q T L A I Y Q Q I L T S L P S R N V I	
3541	CAAATATCGAATGACCTGGAGAACCTCCGGGACCTTCTCCACCTGCTGGCCTCTCCAAG	3600
	Q I S N D L E N L R D L L H L L A S S K	
3601	AGCTGCCCCCTTGCCCAGCAGGGCCTGGAGACCTTGGAGAGCCTGGGCGGCGTCTGGAA	3660
	S C P L P S R A L E T L E S L G G V L E	

F00230"BBE660

FIG. 1C

3661 GCCTCCCTCTACTCCACGGAGGTGGTGGCCCTGAGCAGGCTGCAGGGGGCTCTGCAGGAC 3720
 A S L Y S T E V V A L S R L Q G A L Q D
 3721 ATGCTGCGGCAGCTGGACCTCAGCCCTGGCTGCTGAAGCCTTGAAGGCCTCTCTCCCCAC 3780
 M L R Q L D L S P G C *
 3781 AGTCGGGGGAAGAAACCTGAGCTTCCAGGAGTCTGCTGGAGAAGAGAGCCTGTGCGGACC 3840
 3841 TCCTCTCTGCAGGTCTGCGGACCATTTCTCTCTCGCTCCGCTAAGCTGCTCTTCCAAAGG 3900
 3901 CAGAAAACCTCAAGGCACGACACCAAAGACAGAAAGGCCTGGTTCGCGCGCCACCGGAAA 3960
 3961 GGGGGCGCCGTCCAGCCAACGGTGGACTAGATTTTCGGATTTTCCACCAACGTCTTCCTTC 4020
 4021 CTGTTCCATCTCCAGCTCACCGGTGCTTACGCGTGACCGGGGGGATTTTACAGAGCCTTTC 4080
 4081 GACCATCAAGCAGGGTTCATCTGAGAATTCGGGGAGCACGGTGAAGGCTACAGGCACA 4140
 4141 CACAGCTGGATGCTCCACGCAACACAAGTTGGAAGCATTTCTTTATTTATTATGCGGTG 4200
 4201 TATTCTGGTTGGATTTGAAGCAAAACACCAGCCTTTCCAGGCTCTCTGGGGTCAGCCGGG 4260
 4261 GCTAGGGGGAGGCTCCCGAGGTGCTGTTTCCAGTACCATCCATGGGCCTGCTGAGGCCAA 4320
 4321 CCCATTTTGAGTGACTTGAGGGCTCTCAAGGTCGTTCTCTAGAGACTGGCTTTGTTTCTA 4380
 4381 CTGTGACTGACTTTAAACTGCAGCGTGTGCACTGGCATCGCCTGCGCGGATCTCGAAGG 4440
 4441 GCCAGGTTCTCTTAGAAAGAAGAAGATGAACCTTTGTGAGGGGTGTGTACGCGGAGACAGG 4500
 4501 AAGTGTGTTGGTGGGCGGGGCATGGATCCAGAATGTGTATTTCTTGTGTGATGGACATTT 4560
 4561 GTGTGAGGGGCTCTCTGGACAGGGTGAGGTCATTGTCTCATCTTCGTGGTTTTTCATGAGA 4620
 4621 GAAGGAGATGATTCCTTACGGGGGTCGTGGGGTTTTGCCAGCCGCCCGTGCAGGAGTGG 4680
 4681 GGAAGGGGCTGAAGCCGAAGACCGTTGGGGGCCGTGGTGAGCTCTGCCTTCTCCAGCTGC 4740
 4741 TAGAGGCTGGTCTTTCTCATCAGGGAGTGAGGGTCTCGCGTTGGAGACAGTGATCCCCAG 4800
 4801 GGCGGGATCCTTGCCGTGGCCCTCTGAATGGTCTGGGTGATCCCACACTGATGTCATAAC 4860
 4861 AGGGAAGTGCCCTGGTTTGGGATTTGTATGCTCACCCAAAGCAAGGGCCTGCTTCCCATC 4920
 4921 CATTTTGGGAAGGATTTTTTCTCCAGGGGGAGGGTGAAAGCTCTGGGAGGTCTGTGGGCT 4980
 4981 TACGAGATGGTCCAAGTCCTGGGTGAGTGAGTCCCGGACTCGTGACCGCCTCGAGGAGC 5040
 5041 CCCCTTCTCCCTACAGGTCATGTTCAATAGGTCAAACAAGGAGGCATGGGTTTCCACCAT 5100
 5101 CCTGCCGCTGTGATGCAGCCATCGCACTACAGGAGGTAGATCTGTCCAAGGAAATTTGAA 5160
 5161 TCTCAAGCAATCACTTTCAAGACTGAGCATCTATTGTGCTCAGCCCCAACTGGTGCTATG 5220
 5221 GGCTCAGAGAAGCTCATCAAATAAATATTAAATCCAGTCTGCCTTCAGGACCTTGCAT 5280
 5281 TCCAGATGATAACACCTCCCCACACCCCGTCTGCAGAGGCTGTCATTTACCATGGCAA 5340
 5341 CCGAGCAGCTGAAACACAGTGCGGTCCTCAGCAGGTGGAAAGGCTGAGCTGAGGAGGGCA 5400
 5401 GTGCCCCGGGCCACAGGCTAACCCTGCTTGCACTTGGTAGCATTTTTACTGTTTCGGGGCG 5460
 5461 CATCAGCATCTATTACTGAGAAGCCGCATCCCTTTGAAGCAGGATAGCTGAGACTATAAA 5520
 5521 AATAAGAAAATACCAGAGTTCCTTGTGGCACAGAGGGCTAAGGATCCAGTGTGTTGTGCT 5580
 5581 GCAGCAGCTTGGGTACGGCTGTGGCAAGGGTTCGATCCCTGGCCTGGGAACCTTTCACAT 5640

09932888-082001



5641	GTTGCAGGCAAGGCCAAAAAAATAAATAAAATAAAACAAAAAAACAAGACCA	5700
5701	TAACAGCAGACTGGTGGCAAACCAGGACTAGAACCTGGGTCTCTGACCCCTAGAGTCAG	5760
5761	TGTCCCTGAGCCAGCTAGTGTCTCTGGGGACGGGAACAGGGTTGGGCAGGGAGTTCAG	5820
5821	GAAGTGTTTGCTGGAAGAGCGGAGTTTCCAGGCTGATTTTGCAGGAGGTGAGGGAAGTGG	5880
5881	ATTGCCTGGAGGGAGGAGGCTGTTTTGTTTGAAGCTT	5917

SECRET

FIG. 2

Size 501 , Select 1

1 ATGCGCTGTGGACCCCTGTGCCGATTCCTGCTGGCTTTGGCCTATCTGTCCTACGTTGAA 60

1 M R C G P L C R F L L A L A Y L S Y V E 20

61 GCCGTGCCCATCTGGAGAGTCCAGGATGACACCAAAACCCTCATCAAGACGATTGTCACC 120

21 A V P I W R V Q D D T K T L I K T I V T 40

121 AGGATCAGTGACATTTACACATGCAGTCTGTCTCCTCCAAACAGAGGGTCACCGGTTTG 180

41 R I S D I S H M Q S V S S K Q R V T G L 60

181 GACTTCATCCCTGGGCTCCATCCTGTCCTGAGTTTGTCCAAGATGGACCAGACCCTGGCG 240

61 D F I P G L H P V L S L S K M D Q T L A 80

241 ATCTACCAACAGATCCTCACCAGTCTGCCTTCCAGAAATGTGATCCAAATATCGAATGAC 300

81 I Y Q Q I L T S L P S R N V I Q I S N D 100

301 CTGGAGAACCTCCGGGACCTTCTCCACCTGCTGGCCTCCTCCAAGAGCTGCCCCTTGCCC 360

101 L E N L R D L L H L L A S S K S C P L P 120

361 AGCAGGGCCCTGGAGACCTTGGAGAGCCTGGGCGGCGTCTGGAAGCCTCCCTCTACTCC 420

121 S R A L E T L E S L G G V L E A S L Y S 140

421 ACGGAGGTGGTGGCCCTGAGCAGGCTGCAGGGGGCTCTGCAGGACATGCTGCGGCAGCTG 480

141 T E V V A L S R L Q G A L Q D M L R Q L 160

481 GACCTCAGCCCTGGCTGCTGA 501

161 D L S P G C * 167

09932288-082001

FIG. 3

1	GTGCCCATCTGGAGAGTCCAGGATGACACCAAAACCCTCATCAAGACGATTGTCACCAGG	60
1	V P I W R V Q D D T K T L I K T I V T R	20
61	ATCAGTGACATTTACACATGCAGTCTGTCTCCTCCAAACAGAGGGTCACCGGTTTGGAC	120
21	I S D I S H M Q S V S S K Q R V T G L D	40
121	TTCATCCCTGGGCTCCATCCTGTCCTGAGTTTGTCCAAGATGGACCAGACCCTGGCGATC	180
41	F I P G L H P V L S L S K M D Q T L A I	60
181	TACCAACAGATCCTCACCAGTCTGCCTTCCAGAAATGTGATCCAAATATCGAATGACCTG	240
61	Y Q Q I L T S L P S R N V I Q I S N D L	80
241	GAGAACCTCCGGGACCTTCTCCACCTGCTGGCCTCCTCCAAGAGCTGCCCCCTTGCCCAGC	300
81	E N L R D L L H L L A S S K S C P L P S	100
301	AGGGCCCTGGAGACCTTGGAGAGCCTGGGCGGCGTCCTGGAAGCCTCCCTCTACTCCACG	360
101	R A L E T L E S L G G V L E A S L Y S T	120
361	GAGGTGGTGGCCCTGAGCAGGCTGCAGGGGGCTCTGCAGGACATGCTGCGGCACGTGGAC	420
121	E V V A L S R L Q G A L Q D M L R H V D	140
421	CTCAGCCCTGGCTGC	435
141	L S P G C	145

09932888-082001

FIG. 4

		10	20	30	40	50	
PIG	1	ATGCGCTGTG	GACCCCTGTG	CCGATTCCCTG	CTGGCTTTGG	CC-TATCTGT	50
HUMAN	1	ATGCATTTGG	GAACCCCTGTG	CGGATTCTTG	-TGGCTTTGG	CCCTATCTTT	50
MOUSE	1	ATGTGCTGGA	GACCCCTGTG	TCCGTTTCCTG	-TGGCTTTGG	TCCTATCTGT	50
		60	70	80	90	100	
PIG	51	CCTACGTTGA	AGCCGTGCCC	ATCTGGGAG	TCCAGGATGA	CACCAAAACC	100
HUMAN	51	TCTATGTCCA	AGCTGTGCCC	ATCCAAAAG	TCCAAGATGA	CACCAAAACC	100
MOUSE	51	CTTATGTTCA	AGCAGTGCCCT	ATCCAGAAAG	TCCAGGATGA	CACCAAAACC	100
		110	120	130	140	150	
PIG	101	CTCATCAAGA	CAATTGTCAC	CAGGATCAAT	GACATTTTAC	ACATGCAGTC	150
HUMAN	101	CTCATCAAGA	CAATTGTCAC	CAGGATCAAT	GACATTTTAC	ACACGCAGTC	150
MOUSE	101	CTCATCAAGA	CAATTGTCAC	CAGGATCAAT	GACATTTTAC	ACACGCAGTC	150
		160	170	180	190	200	
PIG	151	TGTCTCCTCC	AAACAGAGGG	TCACCGGTTT	GGACTTCATC	CCTGGGGCTCC	200
HUMAN	151	AGTCTCCTCC	AAACAGAAAG	TCACCGGTTT	GGACTTCATT	CCTGGGGCTCC	200
MOUSE	151	GCTATCCGCC	AAACAGAGGG	TCACGGGCTT	GGACTTCATT	CCTGGGGCTTC	200
		210	220	230	240	250	
PIG	201	ATCCGTGTCCT	GAGTTTGTCC	AAGATGGACC	AGACCTGGCC	GATCTACCAA	250
HUMAN	201	ACCCCATCCCT	GA CCTTATCC	AAGATGGACC	AGACACTGGC	AGTCTACCAA	250
MOUSE	201	ACCCCATCTCT	GAGTTTGTCC	AAGATGGACC	AGACTCTGGC	AGTCTATCAA	250
		260	270	280	290	300	
PIG	251	CAGATCCCTCA	CCAGTCTGCC	TTCCAGAAAT	GTGATCCAA	TATCGAATGA	300
HUMAN	251	CAGATCCCTCA	CCAGTATGCC	TTCCAGAAAC	GTGATCCAA	TATCCAACTGA	300
MOUSE	251	CAGGTCCCTCA	CCAGCTTGCC	TTCCCAAAAT	GTGCTCCAGA	TACCCAATGA	300
		310	320	330	340	350	
PIG	301	CCTGGAGAAG	CTCCGGGACC	TTCTCCACCT	GCTGGCCTTC	TCCAAGAGCT	350
HUMAN	301	CCTGGAGAAG	CTCCGGGATC	TTCTTCACGT	GCTGGCCTTC	TCTAAGAGCT	350
MOUSE	301	CCTGGAGAAAT	CTCCGAGACC	TCCTCCATCT	GCTGGCCTTC	TCCAAGAGCT	350
		360	370	380	390	400	
PIG	351	GGCCCTTGCC	CAG---CAGG	GCCTGGAGA	CCTTGGAGAG	CCTGGGCGGC	400
HUMAN	351	GGCACTTGCC	CTGGGCCAGT	GGCCTGGAGA	CCTTGGACAG	CCTGGGCGGT	400
MOUSE	351	GCTCCCTGCC	TCAGACCAGT	GGCCTGCAGA	AGCCAGAGAG	CCTGGATGGC	400
		410	420	430	440	450	
PIG	401	GTCTTGAAG	CCTGCTCTTA	CTCCACGAG	GTGGTGGCCC	TGAGCAGGCT	450
HUMAN	401	GTCTTGAAG	CTTCAAGGCTA	CTCCACAGAG	GTGGTGGCCC	TGAGCAGGCT	450
MOUSE	401	GTCTTGAAG	CCTCACTCTA	CTCCACAGAG	GTGGTGGCTT	TGAGCAGGCT	450
		460	470	480	490	500	
PIG	451	GCAGGGGGCT	CTGCAGGACA	TGCTGCGGCA	GCTGGACCTC	AGCCCTGGCT	500
HUMAN	451	GCAGGGGTCT	CTGCAGGACA	TGCTGTGGCA	GCTGGACCTC	AGCCCTGGCT	500
MOUSE	451	GCAGGGCTCT	CTGCAGGACA	TTCTTCAACA	GTGGATGTTT	AGCCCTGAAT	500
		510	520	530	540	550	
PIG	501	GCTGA	550
HUMAN	501	GCTGA	550
MOUSE	501	GCTGA	550

099326666-082001

FOO280" 8882E660

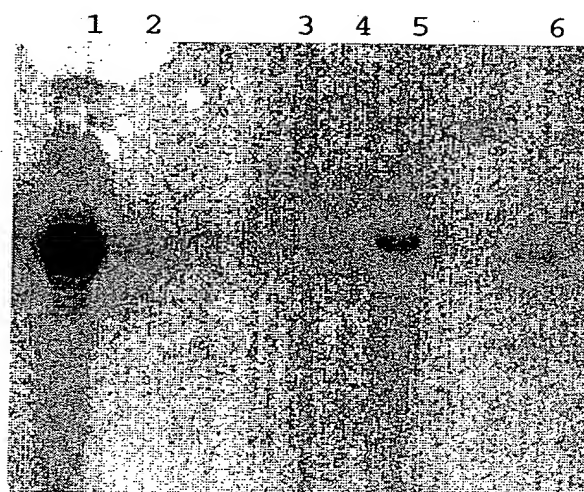


FIG. 5

3

0993288-062001

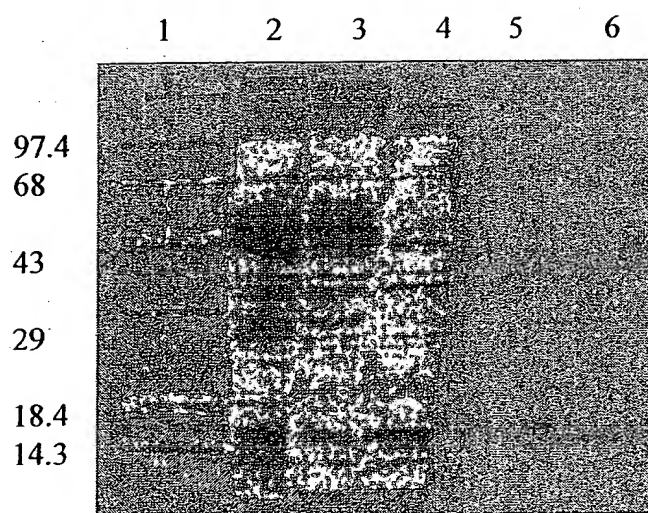
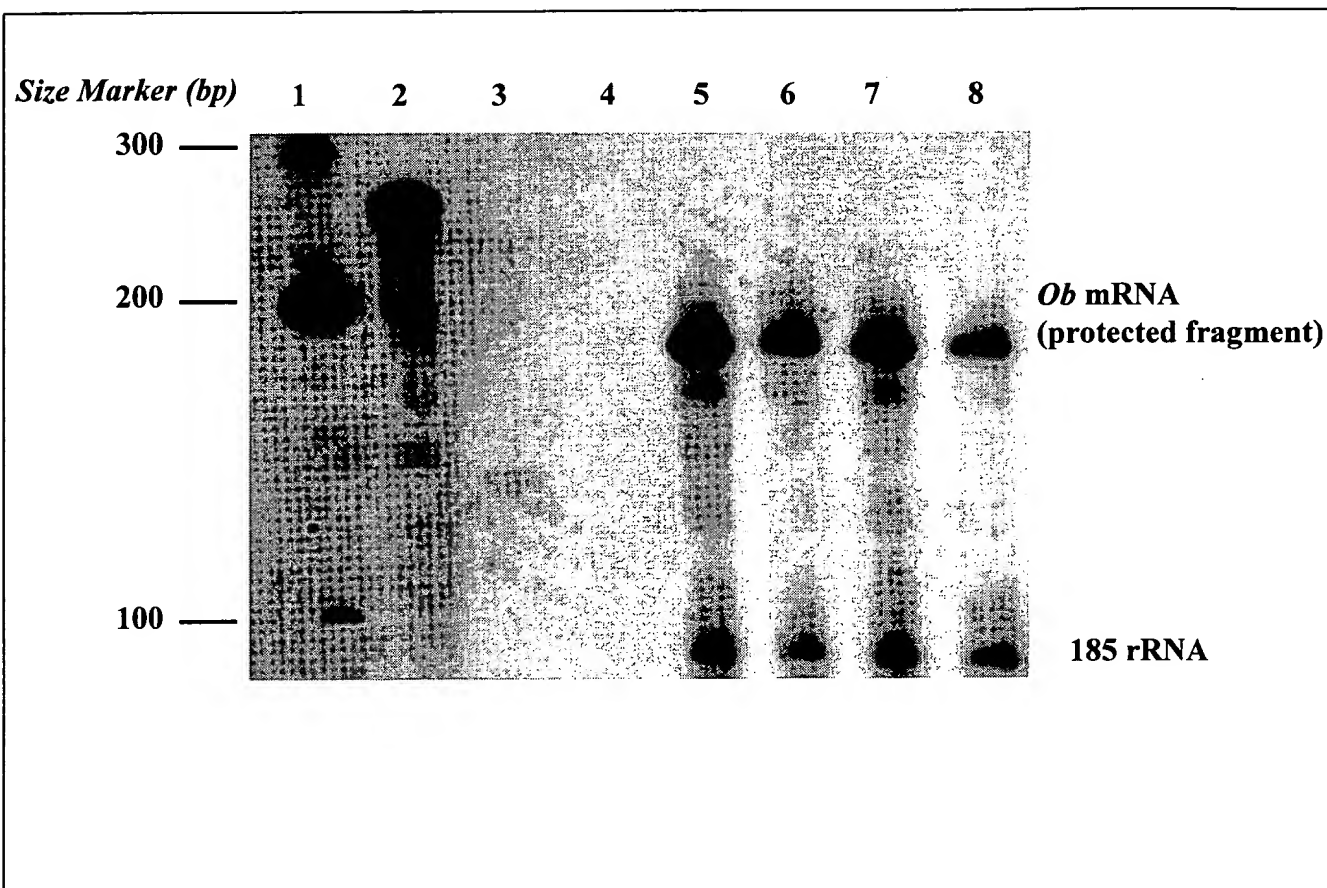


FIG. 7

FIG. 8



FO0220"8832E550

FIG. 9

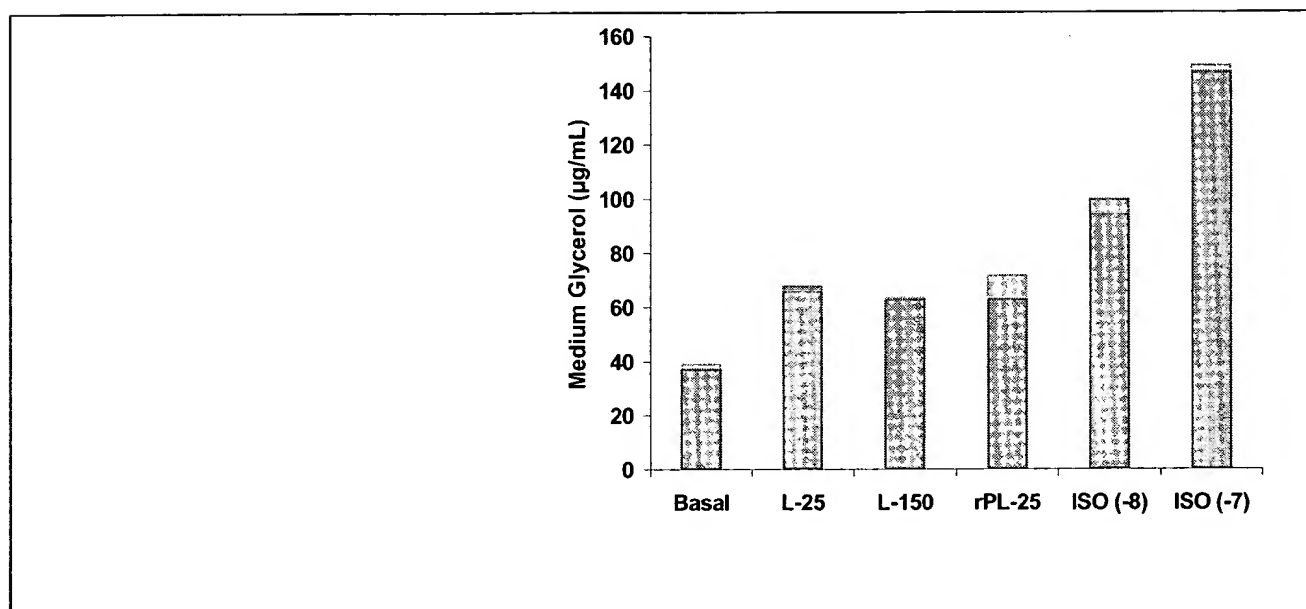
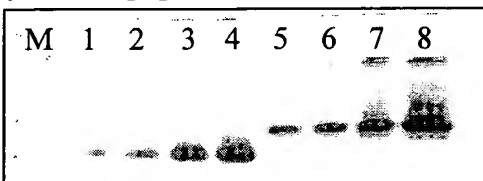


FIG. 10

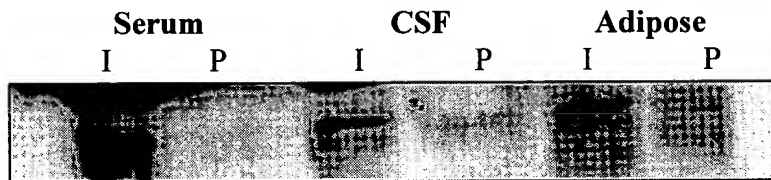
Western blot of recombinant human and porcine leptin with the polyclonal antibody to synthetic peptide based on the C-terminal sequence of porcine leptin.



100230" 8832E660

FIG. 11

A polyclonal antibody to recombinant porcine leptin immunoprecipitates leptin from pig serum, cerebral spinal fluid (CSF), and adipose extracts.



09932888-082001